

RAW SEQUENCE LISTING

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Application Serial Number: 10/553,904
Source: IFWP
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IFWP

RAW SEQUENCE LISTING

DATE: 03/08/2007

PATENT APPLICATION: US/10/553,904

TIME: 12:25:22

Input Set : A:\53694131.APP

Output Set: N:\CRF4\03082007\J553904.raw

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3 <110> APPLICANT: BJORCK, LARS
4     HERWALD, HEIKO
5     MORGELIN, MATTHIAS
6     RUSSELL, WAYNE
7     NORRBY-TEGLUND, ANNA
8     LINDBOM, LENNART
9     SOLLENBERG, ULLA
10    CRAMER, HENNING
11    FLODGAARD, HANS
13 <120> TITLE OF INVENTION: METHOD FOR IDENTIFYING AN ANTI-STREPTOCOCCAL AGENT AND
14    ITS USE FOR TREATING STREPTOCOCCAL INFECTIONS
16 <130> FILE REFERENCE: 053694-0131
18 <140> CURRENT APPLICATION NUMBER: 10/553,904
19 <141> CURRENT FILING DATE: 2005-10-21
21 <150> PRIOR APPLICATION NUMBER: PCT/EP04/004429
22 <151> PRIOR FILING DATE: 2004-04-23
24 <150> PRIOR APPLICATION NUMBER: GB 0309246.7
25 <151> PRIOR FILING DATE: 2003-04-23
27 <150> PRIOR APPLICATION NUMBER: GB 0329112.7
28 <151> PRIOR FILING DATE: 2003-12-16
30 <160> NUMBER OF SEQ ID NOS: 11
32 <170> SOFTWARE: PatentIn Ver. 3.3
34 <210> SEQ ID NO: 1
35 <211> LENGTH: 484
36 <212> TYPE: PRT
37 <213> ORGANISM: Streptococcus pyogenes
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43 Thr Gly Thr Ala Ser Val Ala Val Ala Leu Thr Val Leu Gly Ala Gly
44           20           25           30
46 Phe Ala Asn Gln Thr Glu Val Lys Ala Asn Gly Asp Gly Asn Pro Arg
47           35           40           45
49 Glu Val Ile Glu Asp Leu Ala Ala Asn Asn Pro Ala Ile Gln Asn Ile
50   50           55           60
52 Arg Leu Arg Tyr Glu Asn Lys Asp Leu Lys Ala Arg Leu Glu Asn Ala
53   65           70           75           80
55 Met Glu Val Ala Gly Arg Asp Phe Lys Arg Ala Glu Glu Leu Glu Lys
56           85           90           95
58 Ala Lys Gln Ala Leu Glu Asp Gln Arg Lys Asp Leu Glu Thr Lys Leu
59           100          105          110
61 Lys Glu Leu Gln Gln Asp Tyr Asp Leu Ala Lys Glu Ser Thr Ser Trp
62           115          120          125

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64 Asp Arg Gln Arg Leu Glu Lys Glu Leu Glu Glu Lys Lys Glu Ala Leu
65      130                      135      140
67 Glu Leu Ala Ile Asp Gln Ala Ser Arg Asp Tyr His Arg Ala Thr Ala
68 145                      150                      155                      160
70 Leu Glu Lys Glu Leu Glu Glu Lys Lys Lys Ala Leu Glu Leu Ala Ile
71                      165                      170                      175
73 Asp Gln Ala Ser Gln Asp Tyr Asn Arg Ala Asn Val Leu Glu Lys Glu
74                      180                      185                      190
76 Leu Glu Thr Ile Thr Arg Glu Gln Glu Ile Asn Arg Asn Leu Leu Gly
77      195                      200                      205
79 Asn Ala Lys Leu Glu Leu Asp Gln Leu Ser Ser Glu Lys Glu Gln Leu
80      210                      215                      220
82 Thr Ile Glu Lys Ala Lys Leu Glu Glu Glu Lys Gln Ile Ser Asp Ala
83 225                      230                      235                      240
85 Ser Arg Gln Ser Leu Arg Arg Asp Leu Asp Ala Ser Arg Glu Ala Lys
86                      245                      250                      255
88 Lys Gln Val Glu Lys Asp Leu Ala Asn Leu Thr Ala Glu Leu Asp Lys
89                      260                      265                      270
91 Val Lys Glu Asp Lys Gln Ile Ser Asp Ala Ser Arg Gln Gly Leu Arg
92                      275                      280                      285
94 Arg Asp Leu Asp Ala Ser Arg Glu Ala Lys Lys Gln Val Glu Lys Asp
95      290                      295                      300
97 Leu Ala Asn Leu Thr Ala Glu Leu Asp Lys Val Lys Glu Glu Lys Gln
98 305                      310                      315                      320
100 Ile Ser Asp Ala Ser Arg Gln Gly Leu Arg Arg Asp Leu Asp Ala Ser
101                      325                      330                      335
103 Arg Glu Ala Lys Lys Gln Val Glu Lys Ala Leu Glu Glu Ala Asn Ser
104                      340                      345                      350
106 Lys Leu Ala Ala Leu Glu Lys Leu Asn Lys Glu Leu Glu Glu Ser Lys
107                      355                      360                      365
109 Lys Leu Thr Glu Lys Glu Lys Ala Glu Leu Gln Ala Lys Leu Glu Ala
110      370                      375                      380
112 Glu Ala Lys Ala Leu Lys Glu Gln Leu Ala Lys Gln Ala Glu Glu Leu
113 385                      390                      395                      400
115 Ala Lys Leu Arg Ala Gly Lys Ala Ser Asp Ser Gln Thr Pro Asp Thr
116                      405                      410                      415
118 Lys Pro Gly Asn Lys Ala Val Pro Gly Lys Gly Gln Ala Pro Gln Ala
119                      420                      425                      430
121 Gly Thr Lys Pro Asn Gln Asn Lys Ala Pro Met Lys Glu Thr Lys Arg
122                      435                      440                      445
124 Gln Leu Pro Ser Thr Gly Glu Thr Ala Asn Pro Phe Phe Thr Ala Ala
125      450                      455                      460
127 Ala Leu Thr Val Met Ala Thr Ala Gly Val Ala Ala Val Val Lys Arg
128 465                      470                      475                      480
130 Lys Glu Glu Asn
134 <210> SEQ ID NO: 2
135 <211> LENGTH: 4
136 <212> TYPE: PRT
137 <213> ORGANISM: Artificial Sequence

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139 <220> FEATURE:
140 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
141     peptide
143 <400> SEQUENCE: 2
144 Gly Pro Arg Pro
145     1
148 <210> SEQ ID NO: 3
149 <211> LENGTH: 4
150 <212> TYPE: PRT
151 <213> ORGANISM: Artificial Sequence
153 <220> FEATURE:
154 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
155     peptide
157 <400> SEQUENCE: 3
158 Gly His Arg Pro
159     1
162 <210> SEQ ID NO: 4
163 <211> LENGTH: 13
164 <212> TYPE: DNA
165 <213> ORGANISM: Artificial Sequence
167 <220> FEATURE:
168 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
169     primer
171 <400> SEQUENCE: 4
172 ggggttggtga gaa
175 <210> SEQ ID NO: 5
176 <211> LENGTH: 644
177 <212> TYPE: PRT
178 <213> ORGANISM: Homo sapiens
180 <400> SEQUENCE: 5
181 Met Phe Ser Met Arg Ile Val Cys Leu Val Leu Ser Val Val Gly Thr
182     1             5             10             15
184 Ala Trp Thr Ala Asp Ser Gly Glu Gly Asp Phe Leu Ala Glu Gly Gly
185             20             25             30
187 Gly Val Arg Gly Pro Arg Val Val Glu Arg His Gln Ser Ala Cys Lys
188             35             40             45
190 Asp Ser Asp Trp Pro Phe Cys Ser Asp Glu Asp Trp Asn Tyr Lys Cys
191             50             55             60
193 Pro Ser Gly Cys Arg Met Lys Gly Leu Ile Asp Glu Val Asn Gln Asp
194     65             70             75             80
196 Phe Thr Asn Arg Ile Asn Lys Leu Lys Asn Ser Leu Phe Glu Tyr Gln
197             85             90             95
199 Lys Asn Asn Lys Asp Ser His Ser Leu Thr Thr Asn Ile Met Glu Ile
200             100            105            110
202 Leu Arg Gly Asp Phe Ser Ser Ala Asn Asn Arg Asp Asn Thr Tyr Asn
203             115            120            125
205 Arg Val Ser Glu Asp Leu Arg Ser Arg Ile Glu Val Leu Lys Arg Lys
206             130            135            140
208 Val Ile Glu Lys Val Gln His Ile Gln Leu Leu Gln Lys Asn Val Arg

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209	145				150				155				160			
211	Ala	Gln	Leu	Val	Asp	Met	Lys	Arg	Leu	Glu	Val	Asp	Ile	Asp	Ile	Lys
212					165					170					175	
214	Ile	Arg	Ser	Cys	Arg	Gly	Ser	Cys	Ser	Arg	Ala	Leu	Ala	Arg	Glu	Val
215				180						185					190	
217	Asp	Leu	Lys	Asp	Tyr	Glu	Asp	Gln	Gln	Lys	Gln	Leu	Glu	Gln	Val	Ile
218				195					200					205		
220	Ala	Lys	Asp	Leu	Leu	Pro	Ser	Arg	Asp	Arg	Gln	His	Leu	Pro	Leu	Ile
221		210					215					220				
223	Lys	Met	Lys	Pro	Val	Pro	Asp	Leu	Val	Pro	Gly	Asn	Phe	Lys	Ser	Gln
224	225					230					235					240
226	Leu	Gln	Lys	Val	Pro	Glu	Trp	Lys	Ala	Leu	Thr	Asp	Met	Pro	Gln	
227					245					250					255	
229	Met	Arg	Met	Glu	Leu	Glu	Arg	Pro	Gly	Gly	Asn	Glu	Ile	Thr	Arg	Gly
230				260					265						270	
232	Gly	Ser	Thr	Ser	Tyr	Gly	Thr	Gly	Ser	Glu	Thr	Glu	Ser	Pro	Arg	Asn
233			275					280					285			
235	Pro	Ser	Ser	Ala	Gly	Ser	Trp	Asn	Ser	Gly	Ser	Ser	Gly	Pro	Gly	Ser
236		290					295					300				
238	Thr	Gly	Asn	Arg	Asn	Pro	Gly	Ser	Ser	Gly	Thr	Gly	Gly	Thr	Ala	Thr
239	305					310					315					320
241	Trp	Lys	Pro	Gly	Ser	Ser	Gly	Pro	Gly	Ser	Thr	Gly	Ser	Trp	Asn	Ser
242					325					330					335	
244	Gly	Ser	Ser	Gly	Thr	Gly	Ser	Thr	Gly	Asn	Gln	Asn	Pro	Gly	Ser	Pro
245				340					345					350		
247	Arg	Pro	Gly	Ser	Thr	Gly	Thr	Trp	Asn	Pro	Gly	Ser	Ser	Glu	Arg	Gly
248			355					360					365			
250	Ser	Ala	Gly	His	Trp	Thr	Ser	Glu	Ser	Ser	Val	Ser	Gly	Ser	Thr	Gly
251		370					375					380				
253	Gln	Trp	His	Ser	Glu	Ser	Gly	Ser	Phe	Arg	Pro	Asp	Ser	Pro	Gly	Ser
254	385					390					395					400
256	Gly	Asn	Ala	Arg	Pro	Asn	Asn	Pro	Asp	Trp	Gly	Thr	Phe	Glu	Glu	Val
257					405					410					415	
259	Ser	Gly	Asn	Val	Ser	Pro	Gly	Thr	Arg	Arg	Glu	Tyr	His	Thr	Glu	Lys
260				420					425					430		
262	Leu	Val	Thr	Ser	Lys	Gly	Asp	Lys	Glu	Leu	Arg	Thr	Gly	Lys	Glu	Lys
263			435					440					445			
265	Val	Thr	Ser	Gly	Ser	Thr	Thr	Thr	Thr	Arg	Arg	Ser	Cys	Ser	Lys	Thr
266		450					455					460				
268	Val	Thr	Lys	Thr	Val	Ile	Gly	Pro	Asp	Gly	His	Lys	Glu	Val	Thr	Lys
269	465					470					475				480	
271	Glu	Val	Val	Thr	Ser	Glu	Asp	Gly	Ser	Asp	Cys	Pro	Glu	Ala	Met	Asp
272					485					490					495	
274	Leu	Gly	Thr	Leu	Ser	Gly	Ile	Gly	Thr	Leu	Asp	Gly	Phe	Arg	His	Arg
275				500						505				510		
277	His	Pro	Asp	Glu	Ala	Ala	Phe	Phe	Asp	Thr	Ala	Ser	Thr	Gly	Lys	Thr
278			515					520					525			
280	Phe	Pro	Gly	Phe	Phe	Ser	Pro	Met	Leu	Gly	Glu	Phe	Val	Ser	Glu	Thr
281		530					535					540				

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283 Glu Ser Arg Gly Ser Glu Ser Gly Ile Phe Thr Asn Thr Lys Glu Ser
284 545 550 555 560
286 Ser Ser His His Pro Gly Ile Ala Glu Phe Pro Ser Arg Gly Lys Ser
287 565 570 575
289 Ser Ser Tyr Ser Lys Gln Phe Thr Ser Ser Thr Ser Tyr Asn Arg Gly
290 580 585 590
292 Asp Ser Thr Phe Glu Ser Lys Ser Tyr Lys Met Ala Asp Glu Ala Gly
293 595 600 605
295 Ser Glu Ala Asp His Glu Gly Thr His Ser Thr Lys Arg Gly His Ala
296 610 615 620
298 Lys Ser Arg Pro Val Arg Gly Ile His Thr Ser Pro Leu Gly Lys Pro
299 625 630 635 640
301 Ser Leu Ser Pro
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306 <211> LENGTH: 491
307 <212> TYPE: PRT
308 <213> ORGANISM: Homo sapiens
310 <400> SEQUENCE: 6
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314 His Leu Leu Leu Leu Leu Cys Val Phe Leu Val Lys Ser Gln Gly
315 20 25 30
317 Val Asn Asp Asn Glu Glu Gly Phe Phe Ser Ala Arg Gly His Arg Pro
318 35 40 45
320 Leu Asp Lys Lys Arg Glu Glu Ala Pro Ser Leu Arg Pro Ala Pro Pro
321 50 55 60
323 Pro Ile Ser Gly Gly Gly Tyr Arg Ala Arg Pro Ala Lys Ala Ala Ala
324 65 70 75 80
326 Thr Gln Lys Lys Val Glu Arg Lys Ala Pro Asp Ala Gly Gly Cys Leu
327 85 90 95
329 His Ala Asp Pro Asp Leu Gly Val Leu Cys Pro Thr Gly Cys Gln Leu
330 100 105 110
332 Gln Glu Ala Leu Leu Gln Gln Glu Arg Pro Ile Arg Asn Ser Val Asp
333 115 120 125
335 Glu Leu Asn Asn Asn Val Glu Ala Val Ser Gln Thr Ser Ser Ser Ser
336 130 135 140
338 Phe Gln Tyr Met Tyr Leu Leu Lys Asp Leu Trp Gln Lys Arg Gln Lys
339 145 150 155 160
341 Gln Val Lys Asp Asn Glu Asn Val Val Asn Glu Tyr Ser Ser Glu Leu
342 165 170 175
344 Glu Lys His Gln Leu Tyr Ile Asp Glu Thr Val Asn Ser Asn Ile Pro
345 180 185 190
347 Thr Asn Leu Arg Val Leu Arg Ser Ile Leu Glu Asn Leu Arg Ser Lys
348 195 200 205
350 Ile Gln Lys Leu Glu Ser Asp Val Ser Ala Gln Met Glu Tyr Cys Arg
351 210 215 220
353 Thr Pro Cys Thr Val Ser Cys Asn Ile Pro Val Val Ser Gly Lys Glu
354 225 230 235 240
356 Cys Glu Glu Ile Ile Arg Lys Gly Gly Glu Thr Ser Glu Met Tyr Leu

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VERIFICATION SUMMARY

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